

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Rodier, Patricia M.  
Ingram, Jennifer L.  
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Hyman, Susan L.  
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(ii) TITLE OF INVENTION: GENETIC POLYMORPHISMS WHICH ARE  
ASSOCIATED WITH AUTISM SPECTRUM DISORDERS

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: U.S.A.  
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/049,803  
(B) FILING DATE: 17-JUN-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Goldman, Michael L.  
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(C) REFERENCE/DOCKET NUMBER: 176/60181

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1008 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGACAAATG CAAGAACATGAA CTCCTTCCTG GAATACCCCA TACTTAGCAG TGGCGACTCG 60  
GGGACCTGCT CAGCCCGAGC CTACCCCCTCG GACCATAGGA TTACAACCTTT CCAGTCGTGC 120  
GCGGTCAGCG CCAACAGTTG CGGCGGCGAC GACCAGCTTCC TAGTGGGCAG GGGGGTGCAG 180  
ATCGGTTCGC CCCACCACCA CCACCACAC CACCACCAAC ACCCCCCAGCC GGCTACCTAC 240  
CAGACTTCCG GGAACCTGGG GGTGTCTAC TCCCACCAA GTTGTGGTCC AAGCTATGGC 300  
TCACAGAACT TCAGTGCGCC TTACAGCCCC TACCGTTAA ATCAGGAAGC AGACGTAAGT 360  
GGTGGGTACC CCCAGTGCGC TCCCGCTGTT TACTCTGGAA ATCTCTCATC TCCCATGGTC 420  
CAGCATCACC ACCACCACCA GGGTTATGCT GGGGGCGCGG TGGGCTCGCC TCAATACATT 480  
CACCACTCAT ATGGACAGGA GCACCAGAGC CTGGCCCTGG CTACGTATAA TAACTCCTTG 540  
TCCCCTCTCC ACGCCAGCCA CCAAGAAGCC TGTCGCTCCC CCGCATCGGA GACATCTTCT 600  
CCAGCGCAGA CTTTGACTG GATGAAAGTC AAAAGAAACC CTCCCAAAAC AGGGAAAGTT 660  
GGAGAGTACG GCTACCTGGG TCAACCCAAC GCGGTGCGCA CCAACTTCAC TACCAAGCAG 720  
CTCACGGAAC TGGAGAAGGA GTTCCACTTC AACAAAGTACC TGACGCGCGC CCGCAGGGTG 780  
GAGATCGCTG CATCCCTGCA GCTCAACGAG ACCCAAGTGA AGATCTGGTT CCAGAACCGC 840  
CGAATGAAGC AAAAGAAACG TGAGAAGGAG GGTCTCTTGC CCATCTCTCC GGCCACCCCG 900  
CCAGGAAACG ACGAGAAGGC CGAGGAATCC TCAGAGAAAGT CCAGCTCTTC GCCCTGCGTT 960  
CCTTCCCCGG GGTCTTCTAC CTCAGACACT CTGACTACCT CCCACTGA 1008

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 335 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asp	Asn	Ala	Arg	Met	Asn	Ser	Phe	Leu	Glu	Tyr	Pro	Ile	Leu	Ser
1						5			10				15		
Ser	Gly	Asp	Ser	Gly	Thr	Cys	Ser	Ala	Arg	Ala	Tyr	Pro	Ser	Asp	His
	20					25							30		
Arg	Ile	Thr	Thr	Phe	Gln	Ser	Cys	Ala	Val	Ser	Ala	Asn	Ser	Cys	Gly
	35					40						45			

Gly Asp Asp Arg Phe Leu Val Gly Arg Gly Val Gln Ile Gly Ser Pro  
50 55 60

His His His His His His His His His Pro Gln Pro Ala Thr Tyr  
65 70 75 80

Gln Thr Ser Gly Asn Leu Gly Val Ser Tyr Ser His Ser Ser Cys Gly  
85 90 95

Pro Ser Tyr Gly Ser Gln Asn Phe Ser Ala Pro Tyr Ser Pro Tyr Ala  
100 105 110

Leu Asn Gln Glu Ala Asp Val Ser Gly Gly Tyr Pro Gln Cys Ala Pro  
115 120 125

Ala Val Tyr Ser Gly Asn Leu Ser Ser Pro Met Val Gln His His His  
130 135 140

His His Gln Gly Tyr Ala Gly Gly Ala Val Gly Ser Pro Gln Tyr Ile  
145 150 155 160

His His Ser Tyr Gly Gln Glu His Gln Ser Leu Ala Leu Ala Thr Tyr  
165 170 175

Asn Asn Ser Leu Ser Pro Leu His Ala Ser His Gln Glu Ala Cys Arg  
180 185 190

Ser Pro Ala Ser Glu Thr Ser Ser Pro Ala Gln Thr Phe Asp Trp Met  
195 200 205

Lys Val Lys Arg Asn Pro Pro Lys Thr Gly Lys Val Gly Glu Tyr Gly  
210 215 220

Tyr Leu Gly Gln Pro Asn Ala Val Arg Thr Asn Phe Thr Thr Lys Gln  
225 230 235 240

Leu Thr Glu Leu Glu Lys Glu Phe His Phe Asn Lys Tyr Leu Thr Arg  
245 250 255

Ala Arg Arg Val Glu Ile Ala Ala Ser Leu Gln Leu Asn Glu Thr Gln  
260 265 270

Val Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Gln Lys Lys Arg Glu  
275 280 285

Lys Glu Gly Leu Leu Pro Ile Ser Pro Ala Thr Pro Pro Gly Asn Asp  
290 295 300

Glu Lys Ala Glu Glu Ser Ser Glu Lys Ser Ser Ser Ser Pro Cys Val  
305 310 315 320

Pro Ser Pro Gly Ser Ser Thr Ser Asp Thr Leu Thr Thr Ser His  
325 330 335

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1008 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGACAATG CAAGAACATGAA CTCCTTCCTG GAATACCCCA TACTTAGCAG TGGCGACTCG 60  
GGGACCTGCT CAGCCCGAGC CTACCCCCTCG GACCAGATAGGA TTACAACCTTT CCAGTCGTGC 120  
GCGGTCAGCG CCAACAGTTG CGGCGGCGAC GACCGCTTCC TAGTGGGCAG GGGGGTGCAG 180  
ATCGGTTCGC CCCACCACCA CCACCACAC CACCATGCC ACCCCCCAGCC GGCTACCTAC 240  
CAGACTTCCG GGAACCTGGG GGTGTCTAC TCCCACCAA GTTGTGGTCC AAGCTATGGC 300  
TCACAGAACT TCAGTGCGCC TTACAGCCCC TACCGCTTAA ATCAGGAAGC AGACGTAAGT 360  
GGTGGGTACC CCCAGTGCGC TCCCGCTGTT TACTCTGGAA ATCTCTCATC TCCCATGGTC 420  
CAGCATCACC ACCACCACCA GGGTTATGCT GGGGGCGCGG TGGGCTCGCC TCAATAACATT 480  
CACCACTCAT ATGGACAGGA GCACCAGAGC CTGGCCCTGG CTACGTATAA TAATCCTTG 540  
TCCCCCTCTCC ACGCCAGCCA CCAAGAAGCC TGTCGCTCCC CCGCATCGGA GACATCTTCT 600  
CCAGCGCAGA CTTTGACTG GATGAAAGTC AAAAGAAACC CTCCCAAAAC AGGGAAAGTT 660  
GGAGAGTACG GCTACCTGGG TCAACCCAAC GCGGTGCGCA CCAACTTCAC TACCAAGCAG 720  
CTCACGGAAC TGGAGAAGGA GTTCCACTTC AACAAAGTACC TGACGCGCGC CCGCAGGGTG 780  
GAGATCGCTG CATCCCTGCA GCTCAACGAG ACCCAAGTGA AGATCTGGTT CCAGAACCGC 840  
CGAATGAAGC AAAAGAAACG TGAGAAGGAG GGTCTCTTGC CCATCTCTCC GGCCACCCCG 900  
CCAGGAAACG ACGAGAAGGC CGAGGAATCC TCAGAGAAGT CCAGCTCTTC GCCCTGCGTT 960  
CCTTCCCCGG GGTCTTCTAC CTCAGACACT CTGACTACCT CCCACTGA 1008

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 335 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Asn Ala Arg Met Asn Ser Phe Leu Glu Tyr Pro Ile Leu Ser  
1 5 10 15

Ser Gly Asp Ser Gly Thr Cys Ser Ala Arg Ala Tyr Pro Ser Asp His  
20 25 30

Arg Ile Thr Thr Phe Gln Ser Cys Ala Val Ser Ala Asn Ser Cys Gly  
35 40 45

Gly Asp Asp Arg Phe Leu Val Gly Arg Gly Val Gln Ile Gly Ser Pro  
50 55 60

His His His His His His His Arg His Pro Gln Pro Ala Thr Tyr  
65 70 75 80

Gln Thr Ser Gly Asn Leu Gly Val Ser Tyr Ser His Ser Ser Cys Gly  
85 90 95

Pro Ser Tyr Gly Ser Gln Asn Phe Ser Ala Pro Tyr Ser Pro Tyr Ala  
100 105 110

Leu Asn Gln Glu Ala Asp Val Ser Gly Gly Tyr Pro Gln Cys Ala Pro  
115 120 125

Ala Val Tyr Ser Gly Asn Leu Ser Ser Pro Met Val Gln His His His  
130 135 140

His His Gln Gly Tyr Ala Gly Gly Ala Val Gly Ser Pro Gln Tyr Ile  
145 150 155 160

His His Ser Tyr Gly Gln Glu His Gln Ser Leu Ala Leu Ala Thr Tyr  
165 170 175

Asn Asn Ser Leu Ser Pro Leu His Ala Ser His Gln Glu Ala Cys Arg  
180 185 190

Ser Pro Ala Ser Glu Thr Ser Ser Pro Ala Gln Thr Phe Asp Trp Met  
195 200 205

Lys Val Lys Arg Asn Pro Pro Lys Thr Gly Lys Val Gly Glu Tyr Gly  
210 215 220

Tyr Leu Gly Gln Pro Asn Ala Val Arg Thr Asn Phe Thr Thr Lys Gln  
225 230 235 240

Leu Thr Glu Leu Glu Lys Glu Phe His Phe Asn Lys Tyr Leu Thr Arg  
245 250 255

Ala Arg Arg Val Glu Ile Ala Ala Ser Leu Gln Leu Asn Glu Thr Gln  
260 265 270

Val Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Gln Lys Lys Arg Glu  
275 280 285

Lys Glu Gly Leu Leu Pro Ile Ser Pro Ala Thr Pro Pro Gly Asn Asp  
290 295 300

Glu Lys Ala Glu Glu Ser Ser Glu Lys Ser Ser Ser Ser Pro Cys Val  
305 310 315 320

Pro Ser Pro Gly Ser Ser Thr Ser Asp Thr Leu Thr Thr Ser His  
325 330 335

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1021 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGACGCATGG ACTATAATAG GATGAACTCC TTCTTAGAGT ACCCACTCTG TAACCAGGGGA 60  
CCCAGCGCCT ACAGCGCCCA CAGCGCCCCA ACCTCCTTTC CCCCAAGCTC GGCTCAGGCG 120  
GTTGACAGCT ATGCAAGCGA GGGCCGCTAC GGTGGGGGGC TGTCCAGCCC TGCGTTTCAG 180  
CAGAACTCCG GCTATCCCGC CCAGCAGCCG CCTTCGACCC TGGGGGTGCC CTTCCCCAGC 240  
TCCCGGCCCT CGGGGTATGC TCCTGCCGCC TGCAAGCCCA GCTACGGGCC TTCTCAGTAC 300  
TACCCCTCTGG GTCAATCAGA AGGAGACGGA GGCTATTTC ATCCCTCGAG CTACGGGCC 360  
CAGCTAGGGG GCTTGTCCGA TGGCTACGGA GCAGGGTGGAG CCGGTCCGGG GCCATATCCT 420  
CCGCAGCATC CCCCTTATGG GAACGAGCAG ACCGCGAGCT TTGCACCGGC CTATGCTGAT 480  
CTCCTCTCCG AGGACAAGGA AACACCCTGC CCTTCAGAAC CTAACACCCC CACGGCCCGG 540  
ACCTTCGACT GGATGAAGGT TAAGAGAAC CCACCCAAGA CAGCGAAGGT GTCAGAGCCA 600  
GGCCTGGCT CGCCCAGTGG CCTCCGCACC AACTCACCA CAAGGCAGCT GACAGAACTG 660  
GAAAAGGAGT TCCATTCAA CAAGTACCTG AGCCGGGCC GGAGGGTGGA GATTGCCGCC 720  
ACCCCTGGAGC TCAATGAAAC ACAGGTCAAG ATTTGGTTCC AGAACCGACG AATGAAGCAG 780  
AAGAAGCGCG AGCGAGAGGG AGGTCGGGTC CCCCCAGCCC CACCAGGCTG CCCCCAAGGAG 840  
GCAGCTGGAG ATGCCTCAGA CCAGTCGACA TGCACCTCCC CGGAAGCCTC ACCCAGCTCT 900  
GTCACCTCCT GAACTGAACC TAGCCACCAA TGGGGCTTCC AGGCACCTGGA GCGCCCCAGT 960  
CCAGCCCTAT CCCAGGCTCT CCCAACCCAG GCCTGGCTTC ACTGCCTGGG ATCTCTAGGC 1020  
T 1021

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 301 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Asp Tyr Asn Arg Met Asn Ser Phe Leu Glu Tyr Pro Leu Cys Asn  
1 5 10 15

Arg Gly Pro Ser Ala Tyr Ser Ala His Ser Ala Pro Thr Ser Phe Pro  
20 25 30

Pro Ser Ser Ala Gln Ala Val Asp Ser Tyr Ala Ser Glu Gly Arg Tyr  
35 40 45

Gly Gly Gly Leu Ser Ser Pro Ala Phe Gln Gln Asn Ser Gly Tyr Pro  
50 55 60

Ala Gln Gln Pro Pro Ser Thr Leu Gly Val Pro Phe Pro Ser Ser Ala  
65 70 75 80

Pro Ser Gly Tyr Ala Pro Ala Ala Cys Ser Pro Ser Tyr Gly Pro Ser  
85 90 95

Gln Tyr Tyr Pro Leu Gly Gln Ser Glu Gly Asp Gly Gly Tyr Phe His  
100 105 110

Pro Ser Ser Tyr Gly Ala Gln Leu Gly Gly Leu Ser Asp Gly Tyr Gly  
115 120 125

Ala Gly Gly Ala Gly Pro Gly Pro Tyr Pro Pro Gln His Pro Pro Tyr  
130 135 140

Gly Asn Glu Gln Thr Ala Ser Phe Ala Pro Ala Tyr Ala Asp Leu Leu  
145 150 155 160

Ser Glu Asp Lys Glu Thr Pro Cys Pro Ser Glu Pro Asn Thr Pro Thr  
165 170 175

Ala Arg Thr Phe Asp Trp Met Lys Val Lys Arg Asn Pro Pro Lys Thr  
180 185 190

Ala Lys Val Ser Glu Pro Gly Leu Gly Ser Pro Ser Gly Leu Arg Thr  
195 200 205

Asn Phe Thr Thr Arg Gln Leu Thr Glu Leu Glu Lys Glu Phe His Phe  
210 215 220

Asn Lys Tyr Leu Ser Arg Ala Arg Arg Val Glu Ile Ala Ala Thr Leu  
225 230 235 240

Glu Leu Asn Glu Thr Gln Val Lys Ile Trp Phe Gln Asn Arg Arg Met  
245 250 255

Lys Gln Lys Lys Arg Glu Arg Glu Gly Gly Arg Val Pro Pro Ala Pro  
260 265 270

Pro Gly Cys Pro Lys Glu Ala Ala Gly Asp Ala Ser Asp Gln Ser Thr  
275 280 285

Cys Thr Ser Pro Glu Ala Ser Pro Ser Ser Val Thr Ser  
290 295 300

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1030 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGACGCATGG ACTATAATAG GATGAACTCC TTCTTAGAGT ACCCACTCTG TAACCAGGGGA	60
CCCAGCGCCT ACAGCGCCCA CAGCGCCAC AGCGCCCAA CCTCCTTCC CCCAAGCTCG	120
GCTCAGGCAG TTGACAGCTA TGCAAGCGAG GGCGCTACG GTGGGGGGCT GTCCAGCCCT	180
GCGTTTCAGC AGAACTCCGG CTATCCGCC CAGCAGCCGC CTTCGACCCCT GGGGGTGCCC	240
TTCCCCAGCT CCGCGCCCTC GGGGTATGCT CCTGCCGCCT GCAGCCCCAG CTACGGGCCT	300
TCTCAGTACT ACCCTCTGGG TCAATCAGAA GGAGACGGAG GCTATTTCA TCCCTCGAGC	360
TACGGGGCCC AGCTAGGGGG CTTGTCCGAT GGCTACGGAG CAGGTGGAGC CGGTCCGGGG	420
CCATATCCTC CGCAGCATCC CCCTTATGGG AACGAGCAGA CCGCGAGCTT TGCACCGGCC	480
TATGCTGATC TCCTCTCCGA GGACAAGGAA ACACCCCTGCC CTTCAGAACCC TAACACCCCC	540
ACGGCCCGGA CCTTCGACTG GATGAAGGTT AAGAGAAACC CACCCAAGAC AGCGAAGGTG	600
TCAGAGCCAG GCCTGGGCTC GCCCAGTGGC CTCCGCACCA ACTTCACCAC AAGGCAGCTG	660
ACAGAACTGG AAAAGGAGTT CCATTCAAC AAGTACCTGA GCCGGGCCCG GAGGGTGGAG	720
ATTGCCGCCA CCCTGGAGCT CAATGAAACA CAGGTCAAGA TTTGGTTCCA GAACCGACGA	780
ATGAAGCAGA AGAAGCGCGA GCGAGAGGGA GGTCGGGTCC CCCCAGCCCC ACCAGGCTGC	840
CCCAAGGAGG CAGCTGGAGA TGCCTCAGAC CAGTCGACAT GCACCTCCCC GGAAGCCTCA	900
CCCAGCTCTG TCACCTCCTG AACTGAACCT AGCCACCAAT GGGGCTTCCA GGCACCTGGAG	960
CGCCCCAGTC CAGCCCTATC CCAGGCTCTC CCAACCCAGG CCTGGCTTCA CTGCCTGGGA	1020
TCTCTAGGCT	1030

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 304 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Tyr Asn Arg Met Asn Ser Phe Leu Glu Tyr Pro Leu Cys Asn  
1 5 10 15

Arg Gly Pro Ser Ala Tyr Ser Ala His Ser Ala His Ser Ala Pro Thr  
20 25 30

Ser Phe Pro Pro Ser Ser Ala Gln Ala Val Asp Ser Tyr Ala Ser Glu  
35 40 45

Gly Arg Tyr Gly Gly Leu Ser Ser Pro Ala Phe Gln Gln Asn Ser  
50 55 60

Gly Tyr Pro Ala Gln Gln Pro Pro Ser Thr Leu Gly Val Pro Phe Pro  
65 70 75 80

Ser Ser Ala Pro Ser Gly Tyr Ala Pro Ala Ala Cys Ser Pro Ser Tyr  
85 90 95

Gly Pro Ser Gln Tyr Tyr Pro Leu Gly Gln Ser Glu Gly Asp Gly Gly  
100 105 110

Tyr Phe His Pro Ser Ser Tyr Gly Ala Gln Leu Gly Gly Leu Ser Asp  
115 120 125

Gly Tyr Gly Ala Gly Gly Ala Gly Pro Gly Pro Tyr Pro Pro Gln His  
130 135 140

Pro Pro Tyr Gly Asn Glu Gln Thr Ala Ser Phe Ala Pro Ala Tyr Ala  
145 150 155 160

Asp Leu Leu Ser Glu Asp Lys Glu Thr Pro Cys Pro Ser Glu Pro Asn  
165 170 175

Thr Pro Thr Ala Arg Thr Phe Asp Trp Met Lys Val Lys Arg Asn Pro  
180 185 190

Pro Lys Thr Ala Lys Val Ser Glu Pro Gly Leu Gly Ser Pro Ser Gly  
195 200 205

Leu Arg Thr Asn Phe Thr Thr Arg Gln Leu Thr Glu Leu Glu Lys Glu  
210 215 220

Phe His Phe Asn Lys Tyr Leu Ser Arg Ala Arg Arg Val Glu Ile Ala  
225 230 235 240

Ala Thr Leu Glu Leu Asn Glu Thr Gln Val Lys Ile Trp Phe Gln Asn  
245 250 255

Arg Arg Met Lys Gln Lys Lys Arg Glu Arg Gly Gly Arg Val Pro  
260 265 270

Pro Ala Pro Pro Gly Cys Pro Lys Glu Ala Ala Gly Asp Ala Ser Asp  
275 280 285

Gln Ser Thr Cys Thr Ser Pro Glu Ala Ser Pro Ser Ser Val Thr Ser  
290 295 300

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCATGGACTA TAATAGGATG

20

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCTTGGGTGG GTTTCTCTTA

20